

PATENT
Docket No. 28110/35761A

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant(s): Ford et al.

Serial No: 10/091,085

Filed: March 5, 2002

**For: METHODS AND
MATERIALS RELATING TO
CD39-LIKE POLYPEPTIDES**

Examiner: Phuong N. Huynh


Group: 1644

**CERTIFICATE OF TRANSMISSION
UNDER 37 CFR 1.8**

I hereby certify that this correspondence is being facsimile transmitted to Examiner Phuong N. Huynh, Group Art Unit 1644, Technology Center 1600, facsimile no. 571-273-0846.

Date: September 21, 2004

Person signing Certificate: Renée S. Polizotto


Signature of Person Signing

STATEMENT REGARDING SEQUENCE LISTING UNDER 37 CFR §1.821(f)

Examiner Phuong N. Huynh
Group Art Unit 1644
Technology Center 1600
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Dear Examiner Huynh:

Based on our telephonic discussion on September 21, 2004 regarding the paper copy of the sequence listing for the instant application, a new paper copy of the computer readable copy of the Sequence Listing submitted at the time of filing is submitted herewith. I hereby state that the content of the paper and computer readable copy of the Sequence Listing, submitted in accordance with 37 CFR §1.821(c) and (e), respectively, are the same.

Ford, et al
U.S. Application No. 10/091,085

If the Examiner has any questions regarding this submission or any other questions regarding the instant application, the Examiner is encouraged to contact the undersigned at the telephone number provided below.

Respectfully submitted,

Dated: September 21, 2004

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<110> APPLICANT: Ford, John
 Mulero, Julio
 <120> TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
 POLYPEPTIDES
 <130> FILE REFERENCE: 28110/35761
 <140> CURRENT APPLICATION NUMBER: US/10/091,085
 <141> CURRENT FILING DATE: 2002-03-05
 <150> PRIOR APPLICATION NUMBER: 09/350,836
 <151> PRIOR FILING DATE: 1999-07-09
 <150> PRIOR APPLICATION NUMBER: 09/273,447
 <151> PRIOR FILING DATE: 1999-03-19
 <150> PRIOR APPLICATION NUMBER: 09/118,205
 <151> PRIOR FILING DATE: 1998-07-16
 <150> PRIOR APPLICATION NUMBER: 09/122,449
 <151> PRIOR FILING DATE: 1998-07-24
 <150> PRIOR APPLICATION NUMBER: 09/244,444
 <151> PRIOR FILING DATE: 1999-02-04
 <160> NUMBER OF SEQ ID NOS: 23
 <170> SOFTWARE: PatentIn Ver. 2.0

<210> SEQ ID NO 1
 <211> LENGTH: 300
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
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 gagactgttg ggacorttga cctaggggga gcctccaccc aaatcacgtt cctgccccag 120
 tttgagaaaa ctctggaaca aactcctagg ggctacctca ctctctttga gatgtttaac 180
 agcacttata agctctatac acatagttac ctgggatttg gattgaaagc tgcaagacta 240
 gcaacccttg gagcccttga gacagaaggg actgatgggc acactttccg gagtgcctgt 300

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 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
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 <222> LOCATION: (246)..(1529)
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1718)
 <223> OTHER INFORMATION: n = adenine or guanine or cytosine or thymine
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 tgtggagtgt cttgggtgaa tcttcataca gacaagatca ttatggtgct gttagggttga 120
 aaaagtgata taataaagga acaaaggaga aaattcagaa ggaaagaaaa aattgcctct 180
 gcagggtgtc gagcaggatt gottctgcaa caaaagcctc caccagcca catcttggga 240
 aaaga atg gcc act tct tgg ggc aca gtc ttt ttc atg ctg gtg gta tcc 290
 Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val Ser
 1 5 10 15
 tgt gtt tgc agc gct gtc tcc cac agg aac cag cag act tgg ttt gag 338
 Cys Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu
 20 25 30
 ggt atc ttc ctg tct tcc atg tgc ccc atc aat gtc agc gcc agc acc 386
 Gly Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr
 35 40 45
 ttg tat gga att atg ttt gat gaa ggg agc act gga act cga att cat 434
 Leu Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile His

50	55	60	
ggt tac acc ttt gtg cag aaa atg cca gga cag ctt cca att cta gaa	482		
Val Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu			
65	70	75	
ggg gaa gtt ttt gat tct gtg aag cca gga ctt tct gct ttt gta gat	530		
Gly Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp			
80	85	90	95
caa cct aag cag ggt gct gag acc gtt caa ggg ctc tta gag gtg gcc	578		
Gln Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val Ala			
100	105	110	
aaa gac tca atc ccc cga agt cac tgg aaa aag acc cca gtg gtc cta	626		
Lys Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val Leu			
115	120	125	
aag gca aca gca gga cta cgc tta ctg cca gaa cac aaa gcc aag gct	674		
Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys Ala			
130	135	140	
ctg ctc ttt gag gta aag gag atc ttc agg aag tca cct ttc ctg gta	722		
Leu Leu Phe Glu Val Lys Glu Ile Phe Arg Lys Ser Pro Phe Leu Val			
145	150	155	
cca aag ggc agt gtt agc atc atg gat gga tcc gac gaa ggc ata tta	770		
Pro Lys Gly Ser Val Ser Ile Met Asp Gly Ser Asp Glu Gly Ile Leu			
160	165	170	175
gct tgg gtt act gtg aat ttt ctg aca ggt cag ctg cat ggc cac aga	818		
Ala Trp Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly His Arg			
180	185	190	
cag gag act gtg ggg acc ttg gac cta ggg gga gcc tcc acc caa atc	866		
Gln Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile			
195	200	205	
acg ttc ctg ccc cag ttt gag aaa act ctg gaa caa act cct agg ggc	914		
Thr Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg Gly			
210	215	220	
tac ctc act tcc ttt gag atg ttt aac agc act tat aag ctc tat aca	962		
Tyr Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr Thr			
225	230	235	
cat agt tac ctg gga ttt gga ttg aaa gct gca aga cta gca acc ctg	1010		
His Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr Leu			
240	245	250	255
gga gcc ctg gag aca gaa ggg act gat ggg cac act ttc cgg agt gcc	1058		
Gly Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser Ala			
260	265	270	
tgt tta ccg aga tgg ttg gaa gca gag tgg atc ttt ggg ggt gtg aaa	1106		
Cys Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val Lys			
275	280	285	
tac cag tat ggt ggc aac caa gaa ggg gag gtg ggc ttt gag ccc tgc	1154		
Tyr Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro Cys			
290	295	300	
tat gcc gaa gtg ctg agg gtg gta cga gga aaa ctt cac cag cca gag	1202		
Tyr Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro Glu			
305	310	315	
gag gtc cag aga ggt tcc ttc tat gct ttc tct tac tat tat gac cga	1250		
Glu Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp Arg			
320	325	330	335
gct gtt gac aca gac atg att gat tat gaa aag ggg ggt att tta aaa	1298		
Ala Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu Lys			
340	345	350	
ggt gaa gat ttt gaa aga aaa gcc agg gaa gtg tgt gat aac ttg gaa	1346		
Val Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu Glu			

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          355          360          365
aac ttc acc tca ggc agt oot ttc ctg tgc atg gat ctc agc tac atc 1394
Asn Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr Ile
          370          375          380
aca gcc ctg tta aag gat ggc ttt ggc ttt gca gac agc aca gtc tta 1442
Thr Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val Leu
          385          390          395
cag ctc aca aag aaa gtg aac aac ata gag acg ggc tgg gcc ttg ggg 1490
Gln Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu Gly
          400          405          410          415
gcc acc ttt cac ctg ttg cag tot ctg ggc atc tcc cat tgaggccacg 1539
Ala Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His
          420          425
tacttccttg gagacctgca ttgccaaca cctttttaag gggaggagag agcacttagt 1599
ttctgaacta gtctggggac atcctggact tgagcctaga gattwrgtta attaascgac 1659
cgagcttata cttwatragg taattttactt gcmgtggcgc gtttacacgt cgtgatggna 1719
aacctggcto ccaactaacg cttgasamat ccccttgcca gctgcgatac caaaagccga 1779
cgacgccttc cacagtgcc 1799

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<210> SEQ ID NO 3

<211> LENGTH: 428

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 3

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          20          25          30
Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr Leu
          35          40          45
Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile His Val
          50          55          60
Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu Gly
          65          70          75          80
Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln
          85          90          95
Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val Ala Lys
          100          105          110
Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val Leu Lys
          115          120          125
Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys Ala Leu
          130          135          140
Leu Phe Glu Val Lys Glu Ile Phe Arg Lys Ser Pro Phe Leu Val Pro
          145          150          155          160
Lys Gly Ser Val Ser Ile Met Asp Gly Ser Asp Glu Gly Ile Leu Ala
          165          170          175
Trp Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly His Arg Gln
          180          185          190
Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile Thr
          195          200          205
Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg Gly Tyr
          210          215          220
Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr Thr His
          225          230          235          240
Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr Leu Gly
          245          250          255
Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser Ala Cys

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260	265	270
Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val Lys Tyr		
275	280	285
Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro Cys Tyr		
290	295	300
Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro Glu Glu		
305	310	315
Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp Arg Ala		
325	330	335
Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu Lys Val		
340	345	350
Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu Glu Asn		
355	360	365
Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr Ile Thr		
370	375	380
Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val Leu Gln		
385	390	395
Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu Gly Ala		
405	410	415
Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His		
420	425	

<210> SEQ ID NO 4

<211> LENGTH: 1287

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (1)..(1284)

<400> SEQUENCE: 4

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Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val Ser Cys	
1 5 10 15	
gtt tgc agc gct gtc tcc cac agg aac cag cag act tgg ttt gag ggt	96
Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly	
20 25 30	
atc ttc ctg tct tcc atg tgc ccc atc aat gtc agc gcc agc acc ttg	144
Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr Leu	
35 40 45	
tat gga att atg ttt gat gca ggg agc act gga act cga att cat gtt	192
Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile His Val	
50 55 60	
tac acc ttt gtg cag aaa atg cca gga cag ctt cca att cta gaa ggg	240
Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu Gly	
65 70 75 80	
gaa gtt ttt gat tct gtg aag cca gga ctt tct gct ttt gta gat caa	288
Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln	
85 90 95	
cct aag cag ggt gct gag acc gtt caa ggg ctc tta gag gtg gcc aaa	336
Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val Ala Lys	
100 105 110	
gac tca atc ccc cga agt cac tgg aaa aag acc cca gtg gtc cta aag	384
Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val Leu Lys	
115 120 125	
gca aca gca gga cta cgc tta ctg cca gaa cac aaa gcc aag gct ctg	432
Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys Ala Leu	
130 135 140	

ctc ttt gag gta aag gag atc ttc agg aag tca cct ttc ctg gta cca 480
Leu Phe Glu Val Lys Glu Ile Phe Arg Lys Ser Pro Phe Leu Val Pro
145 150 155 160
aag ggc agt gtt agc atc atg gat gga tcc gac gaa ggc ata tta gct 528
Lys Gly Ser Val Ser Ile Met Asp Gly Ser Asp Glu Gly Ile Leu Ala
165 170 175
tgg gtt act gtg aat ttt ctg aca ggt cag ctg cat ggc cac aga cag 576
Trp Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly His Arg Gln
180 185 190
gag act gtg ggc acc ttg gac cta ggg gga gcc tcc acc caa atc acg 624
Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile Thr
195 200 205
ttc ctg ccc cag ttt gag aaa act ctg gaa caa act cct agg ggc tac 672
Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg Gly Tyr
210 215 220
ctc act tcc ttt gag atg ttt aac agc act tat aag ctc tat aca cat 720
Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr Thr His
225 230 235 240
agt tac ctg gga ttt gga ttg aaa gct gca aga cta gca acc ctg gga 768
Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr Leu Gly
245 250 255
gcc ctg gag aca gaa ggc act gat ggg cac act ttc cgg agt gcc tgt 816
Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser Ala Cys
260 265 270
tta ccg aga tgg ttg gaa gca gag tgg atc ttt ggg ggt gtg aaa tac 864
Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val Lys Tyr
275 280 285
cag tat ggt ggc aac caa gaa ggg gag gtg ggc ttt gag ccc tgc tat 912
Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro Cys Tyr
290 295 300
gcc gaa gtg ctg agg gtg gta cga gga aaa ctt cac cag cca gag gag 960
Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro Glu Glu
305 310 315 320
gtc cag aga ggt tcc ttc tat gct ttc tct tac tat tat gac cga gct 1008
Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp Arg Ala
325 330 335
gtt gac aca gac atg att gat tat gaa aag ggg ggt att tta aaa gtt 1056
Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu Lys Val
340 345 350
gaa gat ttt gaa aga aaa gcc agg gaa gtg tgt gat aac ttg gaa aac 1104
Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu Glu Asn
355 360 365
ttc acc tca ggc agt cct ttc ctg tgc atg gat ctc agc tac atc aca 1152
Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr Ile Thr
370 375 380
gcc ctg tta aag gat ggc ttt ggc ttt gca gac agc aca gtc tta cag 1200
Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val Leu Gln
385 390 395 400
ctc aca aag aaa gtg aac aac ata gag acg ggc tgg gcc ttg ggg gcc 1248
Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu Gly Ala
405 410 415
acc ttt cac ctg ttg cag tct ctg ggc atc tcc cat tga 1287
Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His
420 425

<210> SEQ ID NC 5

<211> LENGTH: 428

<212> TYPE: PRI

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 5

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          20          25          30
Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr Leu
          35          40          45
Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile His Val
          50          55          60
Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu Gly
          65          70          75          80
Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln
          85          90          95
Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val Ala Lys
          100          105          110
Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val Leu Lys
          115          120          125
Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys Ala Leu
          130          135          140
Leu Phe Glu Val Lys Glu Ile Phe Arg Lys Ser Pro Phe Leu Val Pro
          145          150          155          160
Lys Gly Ser Val Ser Ile Met Asp Gly Ser Asp Glu Gly Ile Leu Ala
          165          170          175
Trp Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly His Arg Gln
          180          185          190
Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile Thr
          195          200          205
Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg Gly Tyr
          210          215          220
Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr Thr His
          225          230          235          240
Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr Leu Gly
          245          250          255
Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser Ala Cys
          260          265          270
Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val Lys Tyr
          275          280          285
Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro Cys Tyr
          290          295          300
Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro Glu Glu
          305          310          315          320
Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp Arg Ala
          325          330          335
Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu Lys Val
          340          345          350
Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu Glu Asn
          355          360          365
Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr Ile Thr
          370          375          380
Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val Leu Gln
          385          390          395          400
Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu Gly Ala
          405          410          415
Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His
          420          425

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<210> SEQ ID NO 6
 <211> LENGTH: 1287
 <212> TYPE: DNA
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 <221> NAME/KEY: CDS
 <222> LOCATION: (1)..(1284)
 <400> SEQUENCE: 6

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1 5 10 15
gtt tgc agc gct gtc tcc cac agg aac cag cag act tgg ttt gag ggt 96
Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly
20 25 30
atc ttc ctg tct tcc atg tgc ccc atc aat gtc ago gcc agc acc ttg 144
Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr Leu
35 40 45
tat gga att atg ttt gat gca ggg agc act gga act cga att cat gtt 192
Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile His Val
50 55 60
tac acc ttt gtg cag aaa atg cca gga cag ctt cca att cta gaa ggg 240
Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu Gly
65 70 75 80
gaa gtt ttt gat tct gtg aag cca gga ctt tct gct ttt gta gat caa 288
Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln
85 90 95
cct aag cag ggt gct gag acc gtt caa ggg ctg tta gag gtg gcc aaa 336
Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val Ala Lys
100 105 110
gac tca atc ccc cga agt cac tgg aaa aag acc cca gtg gtc cta aag 384
Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val Leu Lys
115 120 125
gca aca gca gga cta cgc tta ctg cca gaa cac aaa gcc aag gct ctg 432
Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys Ala Leu
130 135 140
ctc ttt gag gta aag gag atc ttc agg aag tca cct ttc ctg gta cca 480
Leu Phe Glu Val Lys Glu Ile Phe Arg Lys Ser Pro Phe Leu Val Pro
145 150 155 160
aag ggc agt gtt agc atc atg act gga caa gac gaa ggc ata ttc gct 528
Lys Gly Ser Val Ser Ile Met Thr Gly Gln Asp Glu Gly Ile Phe Ala
165 170 175
tgg gtt act gtg aat ttt ctg aca ggt cag ctg cat ggc cac aga cag 576
Trp Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly His Arg Gln
180 185 190
gag act gtg ggg acc ttg gac cta ggg gga gcc tcc acc caa atc acg 624
Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile Thr
195 200 205
ttc ctg ccc cag ttt gag aaa act ctg gaa caa act cct agg ggc tac 672
Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg Gly Tyr
210 215 220
ctc act tcc ttt gag atg ttt aac agc act tat aag ctg tat aca cat 720
Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr Thr His
225 230 235 240
agt tac ctg gga ttt gga ttg aaa gct gca aga cta gca acc ctg gga 768
Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr Leu Gly
245 250 255

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gcc ctg gag aca gaa ggg act gat ggg cac act ttc cgg agt gcc tgt      816
Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser Ala Cys
      260      265      270
tta ccg aga tgg ttg gaa gca gag tgg atc ttt ggg ggt gtg aaa tac      864
Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val Lys Tyr
      275      280      285
cag tat ggt ggc aac caa gaa ggg gag gtg ggc ttt gag ccc tgc tat      912
Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro Cys Tyr
      290      295      300
gcc gaa ctg ctg agg gtg gta cga gga aaa ctt cac cag cca gag gag      960
Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro Glu Glu
      305      310      315      320
gtc cag aga ggt tcc ttc tat gct ttc tct tac tat tat gac cga gct      1008
Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp Arg Ala
      325      330      335
gtt gac aca gac atg att gat tat gaa aag ggg ggt att tta aaa gtt      1056
Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu Lys Val
      340      345      350
gaa gat ttt gaa aga aaa gcc agg gaa gtg tgt gat aac ttg gaa aac      1104
Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu Glu Asn
      355      360      365
ttc acc tca ggc agt cct ttc ctg tgc atg gat ctc agc tac atc aca      1152
Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr Ile Thr
      370      375      380
gcc ctg tta aag gat ggc ttt ggc ttt gca gac agc aca gtc tta cag      1200
Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val Leu Gln
      385      390      395      400
ctc aca aag aaa gtg aac aac ata gag acg ggc tgg gcc ttg ggg gcc      1248
Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu Gly Ala
      405      410      415
acc ttt cac ctg ttg cag tot ctg ggc atc tcc cat tga      1287
Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His
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<210> SEQ ID NO 7

<211> LENGTH: 428

<212> TYPE: PR1

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 7

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      20      25      30
Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr Leu
      35      40      45
Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile His Val
      50      55      60
Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu Gly
      65      70      75      80
Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln
      85      90      95
Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val Ala Lys
      100      105      110
Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val Leu Lys
      115      120      125
Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys Ala Leu
      130      135      140

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Leu Phe Glu Val Lys Glu Ile Phe Arg Lys Ser Pro Phe Leu Val Pro
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Lys Gly Ser Val Ser Ile Met Thr Gly Gln Asp Glu Gly Ile Phe Ala
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Trp Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly His Arg Gln
                               180                               185                               190
Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile Thr
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Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg Gly Tyr
210                               215                               220
Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr Thr His
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Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr Leu Gly
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Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser Ala Cys
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275                               280                               285
Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro Cys Tyr
290                               295                               300
Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro Glu Glu
305                               310                               315                               320
Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp Arg Ala
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Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu Lys Val
340                               345                               350
Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu Glu Asn
355                               360                               365
Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr Ile Thr
370                               375                               380
Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val Leu Gln
385                               390                               395                               400
Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu Gly Ala
405                               410                               415
Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His
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<222> LOCATION: (5847)..(5987)
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<222> LOCATION: (9214)
<223> OTHER INFORMATION: n= adenine or guanine or cytosine or thymine
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<223> OTHER INFORMATION: n= adenine or guanine or cytosine or thymine
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<223> OTHER INFORMATION: n= adenine or guanine or cytosine or thymine
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ttt tca tgc tgg tgg tat cct gtg ttt gca gcg ctg tct ccc aca gga 144
acc agc aga ctt ggt ttg agg gta tct tcc tgt ctt cca tgt gcc cca 192
tca atg tca gcg cca gca cct tgt atg gaa tta tgt ttg atg cag gga 240
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<210> SEQ ID NO 11
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<213> ORGANISM: Artificial Sequence
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45

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<213> ORGANISM: Artificial Sequence

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44

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31

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48

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22

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24

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